

SEQUENCE LISTING

<110> Falco, S. Carl
Famodu, Omolayo O.
Lee, Jian-Ming

<120> AROMATIC AMINO ACID BIOSYNTHETIC ENZYMES

<130> BB1299 US NA

<140> US 09/454,279
<141> 1999-12-03

<150> US 60/110,845
<151> 1998-12-04

<160> 22

<170> Microsoft Office 97

<210> 1
<211> 552
<212> DNA
<213> Zea mays

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<222> (513)
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<220>
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 <222> (534)
 <223> n = a, c, g or t

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 tggccttcaa gctgatacacc aagcccgcgg cggcgtcgcc cgctgctgct tactggggag 120
 atctcgcccg ggggcccgcag ggtacgagcc gcgttgccctt cggaccagcg cccaggaaca 180
 aggggctccg cgcggccaac aactccgcaa cgcccatagc taaggtagag agggttgatc 240
 gaagtgacat attgacattg gatagcatca gacaagtttt gattagacta gaagacagca 300
 tcatatttgg ccttttggag agagcacagt tttgttataa tgctgataca tatgatagca 360
 atgctttcca catggatggg tttggaggat cttggttgaa tatagttaga gaactgagaa 420
 gctccatgca caggtggggag ancaagagcc agtganaccn tctttccaag antgctagcc 480
 cgggtgnacta tcannccagg gttgaccatg cgntcatnat anacaaggtt gaangattgg 540
 actctcaaat gg 552

<210> 2
 <211> 93
 <212> PRT
 <213> Zea mays

<400> 2
 Pro Ala Pro Arg Asn Lys Gly Leu Arg Ala Ala Asn Asn Ser Ala Thr
 1 5 10 15
 Pro Ile Ala Lys Val Glu Arg Val Asp Arg Ser Asp Ile Leu Thr Leu
 20 25 30
 Asp Ser Ile Arg Gln Val Leu Ile Arg Leu Glu Asp Ser Ile Ile Phe
 35 40 45
 Gly Leu Leu Glu Arg Ala Gln Phe Cys Tyr Asn Ala Asp Thr Tyr Asp
 50 55 60
 Ser Asn Ala Phe His Met Asp Gly Phe Gly Gly Ser Trp Leu Asn Ile
 65 70 75 80
 Val Arg Glu Leu Thr Glu Lys Leu His Ala Gln Val Gly
 85 90

<210> 3
 <211> 601
 <212> DNA
 <213> Oryza sativa

<220>
 <221> unsure
 <222> (421)
 <223> n = a, c, g or t

<220>
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 <222> (435)
 <223> n = a, c, g or t

<220>
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<220>
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 <222> (490)
 <223> n = a, c, g or t

<220>
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 <222> (507)
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<220>
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 <222> (526)
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<220>
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 <222> (547)
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<220>
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 <223> n = a, c, g or t

<400> 3
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 ccgcgcgccgt ggggatggcc cgcgggggag gaggggccggc cagccgcgtg gagttcgtcc 180
 cgtcgtcgcg gcgggcgcgg ctgcgggcca ccaacaactc cgtcaccccc gtgaccaagg 240
 aggagaaaca gaggatagat caaagtgaat tactgacctt ggacaacatt agaacctcct 300
 tgggttaggca agaagacagc atcatattca gcctcttaga gagagcacag ttttgctaca 360
 aatgctgata tatatgataa aaatgctttc catgttggat ggatttgatg gcctttgggt 420
 naaattcatg gttangagaa aaccgaaaaa ctacatcanc aagtttggga gatacaagag 480
 ccctgatgan caccattctt tccggangat ctgcctgaac aatgtngcaa cctccccagt 540
 atccaanggt ttgcatccaa atggcngatt ccataatann ancaggagat tggaaattat 600
 t 601

<210> 4
 <211> 62
 <212> PRT
 <213> Oryza sativa

<220>
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 <222> (49)
 <223> Xaa = Any Amino Acid

<220>
 <221> UNSURE
 <222> (58)
 <223> Xaa = Any Amino Acid

<400> 4
 Lys Gln Arg Ile Asp Gln Ser Glu Ile Leu Thr Leu Asp Asn Ile Arg
 1 5 10 15
 Thr Ser Leu Val Arg Gln Glu Asp Ser Ile Ile Phe Ser Leu Leu Glu
 20 25 30
 Arg Ala Gln Phe Ala Thr Asn Ala Asp Ile Tyr Asp Lys Asn Ala Phe
 35 40 45
 Xaa Leu Asp Gly Phe Asp Gly Leu Trp Xaa Lys Phe Met Val
 50 55 60

<210> 5
 <211> 525
 <212> DNA
 <213> Glycine max

<220>
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 <222> (432)
 <223> n = a, c, g or t

<220>
 <221> unsure
 <222> (514)
 <223> n = a, c, g or t

<220>
 <221> unsure
 <222> (516)
 <223> n = a, c, g or t

<400> 5
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 acgctagctt ctgtgagaga ggatttggtt aggcaagagg ataccatcat ttatgggtctc 120
 attgagagag ccaagttccc tagcaattct cacacctatg atgaaaagta tgctcaaadc 180
 cagggttttt gtggctcatt ggtggaattt gttgttaaga atacagaggc cattcaagct 240
 aaggctggaa gatacaaaaa ccctgaagaa aacgccttct tcccagaaaa ttaccacca 300
 tcaattgtgc catcttactc cttcaaacag tttttgcac ctggtgctgc ttcaattaac 360
 ataaacaagt catctgggaa aatgtatttc aaagagttac ttccattgct tgctacttcg 420
 ggtgatgatg gnaactatgc gcaaaactgc agctaatac cttcattatt gcagtcattc 480
 ctagaaggat cactatggaa agttttagc tganngnaaa tcagg 525

<210> 6
 <211> 132
 <212> PRT
 <213> Glycine max

<400> 6
 Asp Ser Gly Asn Val Tyr Thr Leu Ala Ser Val Arg Glu Asp Leu Val
 1 5 10 15
 Arg Gln Glu Asp Thr Ile Ile Tyr Gly Leu Ile Glu Arg Ala Lys Phe
 20 25 30
 Pro Ser Asn Ser His Thr Tyr Asp Glu Lys Tyr Ala Gln Ile Gln Gly
 35 40 45
 Phe Cys Gly Ser Leu Val Glu Phe Val Val Lys Asn Thr Glu Ala Ile
 50 55 60
 Gln Ala Lys Ala Gly Arg Tyr Lys Asn Pro Glu Glu Asn Ala Phe Phe
 65 70 75 80
 Pro Glu Asn Leu Pro Pro Ser Ile Val Pro Ser Tyr Ser Phe Lys Gln
 85 90 95
 Phe Leu His Pro Gly Ala Ala Ser Ile Asn Ile Asn Lys Ser Ser Gly
 100 105 110
 Lys Met Tyr Phe Lys Glu Leu Leu Pro Leu Leu Ala Thr Ser Gly Asp
 115 120 125
 Asp Gly Asn Tyr
 130

<210> 7
 <211> 579
 <212> DNA
 <213> Triticum aestivum

<220>
 <221> unsure
 <222> (417)
 <223> n = a, c, g or t

<220>
 <221> unsure
 <222> (484)
 <223> n = a, c, g or t

<220>
 <221> unsure
 <222> (536)
 <223> n = a, c, g or t

<220>
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 <222> (551)
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<220>
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 <222> (565)
 <223> n = a, c, g or t

<220>
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 <222> (577)
 <223> n = a, c, g or t

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 cagaagatgt tccattcttc tctcaagatc ttccaccacc tgtctttcct accaaagggtc 120
 gcccaaagggt tttgcaccct tttgcttcat tggctctgtgt gaatgatgca atatggaaga 180
 tgtatttcaa tgaattgcta ccattattca ctgctggatgg cgatgatggc aactatgcag 240
 aaacagttgc attagatttt gcatgtctgc aggtctcttc aagaagaatt cattgtggca 300
 aatatgttgc tgaggtgaaa ttcaaagacg cgcctcaaga ttatagccca ccaatacgtg 360
 ctaaggacac taatgctctg atgaacttac taacgttcac ggctgttgaa gaaaagggtca 420
 agaagagagt agagaagaag gcaaggatat ttggacagaa tgtcactctg gaggacagtg 480
 taggcaagca agatggtgat gcctgtgaca gtcactgtaa agttgattcc aaagtgcctt 540
 ctaagctata tgatatgtgg ggaatgcctt ttaacgaag 579

<210> 8
 <211> 154
 <212> PRT
 <213> Triticum aestivum

<400> 8
 Glu Phe Phe Val Arg Glu Ala Glu Val Leu His Ala Lys Ala Gly His
 1 5 10 15
 Tyr Gln Lys Pro Glu Asp Val Pro Phe Phe Ser Gln Asp Leu Pro Pro
 20 25 30
 Pro Val Phe Pro Thr Lys Gly Arg Pro Lys Val Leu His Pro Phe Ala
 35 40 45
 Ser Leu Val Cys Val Asn Asp Ala Ile Trp Lys Met Tyr Phe Asn Glu
 50 55 60
 Leu Leu Pro Leu Phe Thr Ala Asp Gly Asp Asp Gly Asn Tyr Ala Glu
 65 70 75 80
 Thr Val Ala Leu Asp Phe Ala Cys Leu Gln Ala Leu Ser Arg Arg Ile
 85 90 95
 His Cys Gly Lys Tyr Val Ala Glu Val Lys Phe Lys Asp Ala Pro Gln
 100 105 110
 Asp Tyr Ser Pro Pro Ile Arg Ala Lys Asp Thr Asn Ala Leu Met Asn
 115 120 125
 Leu Leu Thr Phe Thr Ala Val Glu Glu Lys Val Lys Lys Arg Val Glu
 130 135 140
 Lys Lys Ala Arg Ile Phe Gly Gln Asn Val
 145 150

<210> 9
 <211> 550
 <212> DNA
 <213> Glycine max

 <220>
 <221> unsure
 <222> (328)
 <223> n = a, c, g or t

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 ctcacgcaaaa gctcctgaga tagcagcatt tgagaaatat ctacctcctg atgttgaaat 60
 cgtatcttgc cattccctcc acggtcccaa tgttgatcct cgaggtcaac ctcttgtctt 120
 gatcaaacat cgtgcttctc aagaaagttt cgaaaaagtc gagcatgtac tctcctgcct 180
 cggctccaaa cagcatgtcc tctcagcatc tcagcacgac cgtatcacag cagataccca 240
 agccgtcacc catgcagcct tcctatccat gggtaaagcc tggcacgcca accttcaatt 300
 tccctgggag atagcccgtt acgttggnngg tatcgaaaac gtcaaaatca atctgactct 360
 tcgtatttat tctcaaaaat ggcatgtcta cgccgggtctc gccatcctga acccttatgc 420
 caaagaacag attagagagt atgcacaaaag cgtgacaaga tctatataag ttgatgctgg 480
 gagggcaccg aagagagcta gaagaagcga atcaagagtg caggacgatt tgtctttgct 540
 gggcgcaaaa 550

<210> 10
 <211> 152
 <212> PRT
 <213> Glycine max

<400> 10
 Ser Cys Lys Ala Pro Glu Ile Ala Ala Phe Glu Lys Tyr Leu Pro Pro
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 Asp Val Glu Ile Val Ser Cys His Ser Leu His Gly Pro Asn Val Asp
 20 25 30

 Pro Arg Gly Gln Pro Leu Val Leu Ile Lys His Arg Ala Ser Gln Glu
 35 40 45

 Ser Phe Glu Lys Val Glu His Val Leu Ser Cys Leu Gly Ser Lys Gln
 50 55 60

 His Val Leu Ser Ala Ser Gln His Asp Arg Ile Thr Ala Asp Thr Gln
 65 70 75 80

 Ala Val Thr His Ala Ala Phe Leu Ser Met Gly Lys Ala Trp His Ala
 85 90 95

 Asn Leu Gln Phe Pro Trp Glu Ile Ala Arg Tyr Val Gly Gly Ile Glu
 100 105 110

 Asn Val Lys Ile Asn Leu Thr Leu Arg Ile Tyr Ser Gln Lys Trp His
 115 120 125

 Val Tyr Ala Gly Leu Ala Ile Leu Asn Pro Tyr Ala Lys Glu Gln Ile
 130 135 140

 Arg Glu Tyr Ala Gln Ser Val Thr
 145 150

<210> 11
 <211> 1223
 <212> DNA
 <213> Zea mays

<400> 11
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 tggccttcaa gctgaccacc aagcccgcgg cggcgctgcc cgctgctgct tactggggag 120
 atctcgcccg ggggcccag ggtacgagcc gcgttgccct cggaccagcg cccaggaaca 180
 aggggctccg cgcggccaac aactccgcaa cgcccatagc taaggtagag agggttgatc 240
 gaagtgcacat attgacattg gatagcatca gacaagtttt gattagacta gaagacagca 300
 tcatatttgg ccttttggag agagcacagt tttgttacia tgctgataca tatgatagca 360
 atgctttcca catggatggg tttggaggat ctttggttga atatatagtt agagaaactg 420
 aaaagctcca tgcacagggt gggagataca agagcccaga tgagcaccct ttcttttcca 480
 aggatctgcc tgagccccgg ttgccaccta tgcaataccc aagggttttg catcccattg 540
 ctgattctat caatatcaac aaagagattt ggaaaatgta ttttgatgaa cttcttccaa 600
 gattggtgaa agaaggaagt gatggtaatg ctggatccag tgctctttgt gacacaacct 660
 gcttgaggc actctccaga aggatccact atgggaagtt tgtggcagag gccaagtttc 720
 aagagtcccc tgaagcttac acgccagcca taatagccca agaccgtgat caactcatga 780
 accttctcac atatgaaacg gtggagcgtg ctatcgaaca cagggtggag gccaaagcca 840
 agatcttcgg gcaagagggt aacattgggt ctaaggacaa cggcagccca cgggtctaca 900
 aaatcaggcc gagcttggtc gccgagctgt acagctacag aatcatgccg ctaaccaagg 960
 aggttgaggt cgcgtacttg ctttaaggagc tggattgagt gtgtttacgt agctgtaaaa 1020
 ctgccagatc cgaactcctg gtattaaacc ataacatcgg taagtaccca tttctgtgaa 1080
 gaggatgatc cgaactcctg tcattaaacc agaacatcag taagtaccca gttttgggga 1140
 gaggatggaa aatataccat gtgtggcaag caacatgcat aatatcatct ggagttgcgc 1200
 ttaaaaaaaaa aaaaaaaaa aac 1223

<210> 12
 <211> 331
 <212> PRT
 <213> Zea mays

<400> 12
 Ala Phe Ser Leu Pro Asn Val Leu Ser Leu Pro Phe Pro Ala Arg Trp
 1 5 10 15
 Leu Val Ala Met Ala Phe Lys Leu Ile Thr Lys Pro Ala Ala Ala Ser
 20 25 30
 Pro Ala Ala Ala Tyr Trp Gly Asp Leu Ala Arg Gly Pro Gln Gly Thr
 35 40 45
 Ser Arg Val Ala Phe Gly Pro Ala Pro Arg Asn Lys Gly Leu Arg Ala
 50 55 60
 Ala Asn Asn Ser Ala Thr Pro Ile Ala Lys Val Glu Arg Val Asp Arg
 65 70 75 80
 Ser Asp Ile Leu Thr Leu Asp Ser Ile Arg Gln Val Leu Ile Arg Leu
 85 90 95
 Glu Asp Ser Ile Ile Phe Gly Leu Leu Glu Arg Ala Gln Phe Cys Tyr
 100 105 110
 Asn Ala Asp Thr Tyr Asp Ser Asn Ala Phe His Met Asp Gly Phe Gly
 115 120 125
 Gly Ser Leu Val Glu Tyr Ile Val Arg Glu Thr Glu Lys Leu His Ala
 130 135 140

Gln Val Gly Arg Tyr Lys Ser Pro Asp Glu His Pro Phe Phe Ser Lys
 145 150 155 160
 Asp Leu Pro Glu Pro Arg Leu Pro Pro Met Gln Tyr Pro Arg Val Leu
 165 170 175
 His Pro Ile Ala Asp Ser Ile Asn Ile Asn Lys Glu Ile Trp Lys Met
 180 185 190
 Tyr Phe Asp Glu Leu Leu Pro Arg Leu Val Lys Glu Gly Ser Asp Gly
 195 200 205
 Asn Ala Gly Ser Ser Ala Leu Cys Asp Thr Thr Cys Leu Gln Ala Leu
 210 215 220
 Ser Arg Arg Ile His Tyr Gly Lys Phe Val Ala Glu Ala Lys Phe Gln
 225 230 235 240
 Glu Ser Pro Glu Ala Tyr Thr Pro Ala Ile Ile Ala Gln Asp Arg Asp
 245 250 255
 Gln Leu Met Asn Leu Leu Thr Tyr Glu Thr Val Glu Arg Ala Ile Glu
 260 265 270
 His Arg Val Glu Ala Lys Ala Lys Ile Phe Gly Gln Glu Val Asn Ile
 275 280 285
 Gly Ala Lys Asp Asn Gly Ser Pro Pro Val Tyr Lys Ile Arg Pro Ser
 290 295 300
 Leu Val Ala Glu Leu Tyr Ser Tyr Arg Ile Met Pro Leu Thr Lys Glu
 305 310 315 320
 Val Glu Val Ala Tyr Leu Leu Lys Arg Leu Asp
 325 330

<210> 13
 <211> 1231
 <212> DNA
 <213> *Oryza sativa*

<400> 13
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 ccattgcgcg cgagcgtgcg agctatggag ttcaacaagg tggctctccag ctacagggcc 120
 gcctcgcccg cgcccggtgg gatggccgc gggggaggag ggccggccag ccgctggag 180
 ttctgcccgt cgtcgcggcg ggcgcggctc gcggccacca acaactccgt caccctcgtg 240
 accaaggagg agaaacagag gatagatcaa agtgaaatac tgaccttga caacattaga 300
 acctccttgg ttaggcaaga agacagcatc atattcagcc tcttagagag agcacagttt 360
 tgctacaatg ctgatata tgataaaaat gctttccatg tggatggatt tgatggctct 420
 ttggttgaat tcatggttag agaaaccgaa aaactacatc aacaggttgg gagatacaag 480
 agcctgatg agcaccatt ctttcggag gatctgcctg aaccactgtt gccacctctc 540
 cagtatccaa aggttttgca tcctattgct gattctatta atatcaacaa ggagatttgg 600
 aaaatgtatt ttgatgagct tcttccaaga ttagtgaaag aaggaagtga tggtaattat 660
 ggatccagtg ctctttgtga cacgatctgc ttgcaggcgc tctccaaaag aattcactat 720
 ggtaagtgtg tggcagaggc taagtttcaa gagtctcctg aagcttacat gcctgcgata 780
 atagcacagg actgcgatca actaatgcac ctcctcacct atgaaacggg ggagcgtgct 840
 attgaacata ggggtggaagc taaggctaag atctttggac aggaggtgga ttaggcgct 900
 gaagacaacg gcgctccacc aatgtacaag ataaggccca gtttggtggc tgaactgtac 960
 agctacagga tcatgccgct aaccaaggag gttcaagtag cctacttgct gaggagattg 1020

gattgattgt ttacgattgt aaactgccag cttcggtttc ctggcatcaa agaataaatt 1080
 aggggaaaga caaccatagg tatccatttt gggacaactg aaagaaaata ttttattcgg 1140
 gtttacacta tattttgtgg caagaacaag cagaagcagg atatcacatg aaatgatatg 1200
 gagatgttgc atataaaaaa aaaaaaaaaa a 1231

<210> 14
 <211> 257
 <212> PRT
 <213> Oryza sativa

<400> 14
 Lys Gln Arg Ile Asp Gln Ser Glu Ile Leu Thr Leu Asp Asn Ile Arg
 1 5 10 15
 Thr Ser Leu Val Arg Gln Glu Asp Ser Ile Ile Phe Ser Leu Leu Glu
 20 25 30
 Arg Ala Gln Phe Cys Tyr Asn Ala Asp Ile Tyr Asp Lys Asn Ala Phe
 35 40 45
 His Val Asp Gly Phe Asp Gly Ser Leu Val Glu Phe Met Val Arg Glu
 50 55 60
 Thr Glu Lys Leu His Gln Gln Val Gly Arg Tyr Lys Ser Pro Asp Glu
 65 70 75 80
 His Pro Phe Phe Pro Glu Asp Leu Pro Glu Pro Leu Leu Pro Pro Leu
 85 90 95
 Gln Tyr Pro Lys Val Leu His Pro Ile Ala Asp Ser Ile Asn Ile Asn
 100 105 110
 Lys Glu Ile Trp Lys Met Tyr Phe Asp Glu Leu Leu Pro Arg Leu Val
 115 120 125
 Lys Glu Gly Ser Asp Gly Asn Tyr Gly Ser Ser Ala Leu Cys Asp Thr
 130 135 140
 Ile Cys Leu Gln Ala Leu Ser Lys Arg Ile His Tyr Gly Lys Phe Val
 145 150 155 160
 Ala Glu Ala Lys Phe Gln Glu Ser Pro Glu Ala Tyr Met Pro Ala Ile
 165 170 175
 Ile Ala Gln Asp Cys Asp Gln Leu Met His Leu Leu Thr Tyr Glu Thr
 180 185 190
 Val Glu Arg Ala Ile Glu His Arg Val Glu Ala Lys Ala Lys Ile Phe
 195 200 205
 Gly Gln Glu Val Asp Leu Gly Ala Glu Asp Asn Gly Ala Pro Pro Met
 210 215 220
 Tyr Lys Ile Arg Pro Ser Leu Val Ala Glu Leu Tyr Ser Tyr Arg Ile
 225 230 235 240
 Met Pro Leu Thr Lys Glu Val Gln Val Ala Tyr Leu Leu Arg Arg Leu
 245 250 255

Asp

<210> 15
 <211> 1020
 <212> DNA
 <213> Glycine max

<400> 15
 gcacgagagc ttaatttcaa gaatggccaa agcagcagaa caaagtcctg attctgggaa 60
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 tgggtctcatt gagagagcca agttccctag caattctcac acctatgatg aaaagtatgc 180
 tcaaatccag ggtttttgtg gctcattggg ggaatttgtt gttaagaata cagaggccat 240
 tcaagctaag gctggaagat acaaaaaccc tgaagaaaac gccttcttcc cagaaaattt 300
 accaccatca attgtgccat cttactcctt caaacagttt ttgcatcctg gtgctgcttc 360
 aattaacata aacaagtcca tctggaaaat gtatttcaaa gagttacttc cattgcttgc 420
 tacttcgggt gatgatggca actatgcgca aactgcagct aatgaccttt cattattgca 480
 gtccatctct agaaggattc actatggaaa gttttagctg gaggtgaaat tcagggatgc 540
 tcctcaagac tacgagcctt taattcgagc taaggataaa gaaggattga tgaaattgtt 600
 gacatttaca agcgttgaag agacggtgag gaagagagtt gaaaagaagg ctgtggtgtt 660
 tgggcaggaa gtgaatctta acagtgatga caatgacaat gaaaaccgta aatttgatcc 720
 atcagtggct tctagcttgt acaaaaattg ggtgatacct ctcaccaagg aggttcaggt 780
 tgagtacctc ttgcgcgctc tagactgaag gcattacaat gcagttagaa tttagaagaa 840
 tggaagatga atatgatgtt gttgttcaaa tgattaagct cttaagtgat cctttattgc 900
 caacttcatg tagctgttga ttcagaaata ttattttagt ctatagattg ttacctttat 960
 tttcatcggc tttattagga aaaggcatta ttatatcatg atcttcaaaa aaaaaaaaaa 1020

<210> 16
 <211> 261
 <212> PRT
 <213> Glycine max

<400> 16
 Met Ala Lys Ala Ala Glu Gln Ser Pro Asp Ser Gly Asn Val Tyr Thr
 1 5 10 15
 Leu Ala Ser Val Arg Glu Asp Leu Val Arg Gln Glu Asp Thr Ile Ile
 20 25 30
 Tyr Gly Leu Ile Glu Arg Ala Lys Phe Pro Ser Asn Ser His Thr Tyr
 35 40 45
 Asp Glu Lys Tyr Ala Gln Ile Gln Gly Phe Cys Gly Ser Leu Val Glu
 50 55 60
 Phe Val Val Lys Asn Thr Glu Ala Ile Gln Ala Lys Ala Gly Arg Tyr
 65 70 75 80
 Lys Asn Pro Glu Glu Asn Ala Phe Phe Pro Glu Asn Leu Pro Pro Ser
 85 90 95
 Ile Val Pro Ser Tyr Ser Phe Lys Gln Phe Leu His Pro Gly Ala Ala
 100 105 110
 Ser Ile Asn Ile Asn Lys Ser Ile Trp Lys Met Tyr Phe Lys Glu Leu
 115 120 125
 Leu Pro Leu Leu Ala Thr Ser Gly Asp Asp Gly Asn Tyr Ala Gln Thr
 130 135 140

Ala Ala Asn Asp Leu Ser Leu Leu Gln Ser Ile Ser Arg Arg Ile His
145 150 155 160

Tyr Gly Lys Phe Val Ala Glu Val Lys Phe Arg Asp Ala Pro Gln Asp
165 170 175

Tyr Glu Pro Leu Ile Arg Ala Lys Asp Lys Glu Gly Leu Met Lys Leu
180 185 190

Leu Thr Phe Thr Ser Val Glu Glu Thr Val Arg Lys Arg Val Glu Lys
195 200 205

Lys Ala Val Val Phe Gly Gln Glu Val Asn Leu Asn Ser Asp Asp Asn
210 215 220

Asp Asn Glu Asn Arg Lys Phe Asp Pro Ser Val Ala Ser Ser Leu Tyr
225 230 235 240

Lys Asn Trp Val Ile Pro Leu Thr Lys Glu Val Gln Val Glu Tyr Leu
245 250 255

Leu Arg Arg Leu Asp
260

<210> 17
<211> 780
<212> DNA
<213> Triticum aestivum

<400> 17
gcacgagccg agttcttcgt tcgggaagcc gaggtcctgc acgccaaggc tggacactat 60
caaaagccag aagatgttcc attcttctct caagatcttc caccacctgt ctttcctacc 120
aaaggctgcc caaagggttt gcaccctttt gcttcattgg tctgtgtgaa tgatgcaata 180
tggaagatgt atttcaatga attgctacca ttattcactg cggatggcga tgatggcaac 240
tatgcagaaa cagttgcatt agattttgca tgtctgcagg ctctctcaag aagaattcat 300
tgtggcaaat atgttgctga ggtgaaattc aaagacgcgc ctcaagatta tagcccacca 360
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Pro Phe Ala Ser Leu Val Cys Val Asn Asp Ala Ile Trp Lys Met Tyr
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 Phe Asn Glu Leu Leu Pro Leu Phe Thr Ala Asp Gly Asp Asp Gly Asn
 65 70 75 80
 Tyr Ala Glu Thr Val Ala Leu Asp Phe Ala Cys Leu Gln Ala Leu Ser
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 Arg Arg Ile His Cys Gly Lys Tyr Val Ala Glu Val Lys Phe Lys Asp
 100 105 110
 Ala Pro Gln Asp Tyr Ser Pro Pro Ile Arg Ala Lys Asp Thr Asn Ala
 115 120 125
 Leu Met Asn Leu Leu Thr Phe Thr Ala Val Glu Glu Lys Val Lys Lys
 130 135 140
 Arg Val Glu Lys Lys Ala Arg Ile Phe Gly Gln Asn Val Thr Leu Glu
 145 150 155 160
 Asp Ser Val Gly Lys Gln Asp Gly Asp Ala Cys Asp Ser His Cys Lys
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 Val Asp Pro Lys Val Leu Ser Lys Leu Tyr Asp Met Trp Val Met Pro
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 <212> DNA
 <213> Glycine max

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 <211> 332
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<400> 20

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			20					25					30		
Val	Asp	Pro	Arg	Gly	Gln	Pro	Leu	Val	Leu	Ile	Lys	His	Arg	Ala	Ser
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Gln	Glu	Ser	Phe	Glu	Lys	Val	Glu	His	Val	Leu	Ser	Cys	Leu	Gly	Ser
	50					55					60				
Lys	Gln	His	Val	Leu	Ser	Ala	Ser	Gln	His	Asp	Arg	Ile	Thr	Ala	Asp
65					70					75					80
Thr	Gln	Ala	Val	Thr	His	Ala	Ala	Phe	Leu	Ser	Met	Gly	Lys	Ala	Trp
				85					90					95	
His	Ala	Asn	Leu	Gln	Phe	Pro	Trp	Glu	Ile	Ala	Arg	Tyr	Val	Gly	Gly
			100					105					110		
Ile	Glu	Asn	Val	Lys	Ile	Asn	Leu	Thr	Leu	Arg	Ile	Tyr	Ser	Gln	Lys
		115					120					125			
Trp	His	Val	Tyr	Ala	Gly	Leu	Ala	Ile	Leu	Asn	Pro	Tyr	Ala	Lys	Glu
	130					135					140				
Gln	Ile	Arg	Glu	Tyr	Ala	Gln	Ser	Val	Thr	Asp	Leu	Tyr	Lys	Leu	Met
145					150					155					160
Leu	Gly	Gly	His	Arg	Arg	Glu	Leu	Glu	Glu	Arg	Ile	Lys	Ser	Ala	Gly
			165					170						175	
Arg	Phe	Val	Phe	Ala	Gly	Arg	Lys	Lys	Ser	Asp	Glu	Leu	Leu	Leu	Arg
			180					185					190		
Asp	Glu	Val	Leu	Asp	Arg	Phe	Ser	Leu	Gly	Lys	Lys	Pro	Glu	Lys	Pro
	195						200					205			
Thr	Pro	Asn	Asn	His	Leu	Ser	Leu	Leu	Ala	Ile	Val	Asp	Cys	Trp	Ala
	210					215					220				
Arg	Leu	Asn	Ile	Ile	Pro	Tyr	Asp	His	Met	Ile	Cys	Ser	Thr	Pro	Leu
225					230					235					240
Phe	Arg	Leu	Trp	Leu	Gly	Val	Ser	Glu	Tyr	Leu	Phe	Arg	Asn	Glu	Lys
			245						250					255	
Leu	Leu	Asp	Glu	Val	Ile	Asn	Thr	Ala	Ile	Glu	Asp	Asn	Thr	Phe	Arg
		260						265					270		
Ser	Asp	Asp	Leu	Glu	Phe	Thr	Phe	Ala	Ala	Arg	Gly	Trp	Ser	Glu	Cys
		275					280					285			

Val Glu Phe Gly Asp Phe Glu Ser Trp Lys Asp Arg Phe Glu Lys Thr
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 Gln Met Phe Phe Ala Pro Arg Phe Pro Glu Ala Thr Arg Val Gly Asn
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 325 330
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 35 40 45
 Ser Lys Pro Arg Ser Gly Thr Ser Ser Val His Ala Val Met Thr Leu
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 Ala Gly Ser Leu Thr Gly Lys Lys Arg Val Asp Glu Ser Glu Ser Leu
 65 70 75 80
 Thr Leu Glu Gly Ile Arg Asn Ser Leu Ile Arg Gln Glu Asp Ser Ile
 85 90 95
 Ile Phe Gly Leu Leu Glu Arg Ala Lys Tyr Cys Tyr Asn Ala Asp Thr
 100 105 110
 Tyr Asp Pro Thr Ala Phe Asp Met Asp Gly Phe Asn Gly Ser Leu Val
 115 120 125
 Glu Tyr Met Val Lys Gly Thr Glu Lys Leu His Ala Lys Val Gly Arg
 130 135 140
 Phe Lys Ser Pro Asp Glu His Pro Phe Phe Pro Asp Asp Leu Pro Glu
 145 150 155 160
 Pro Met Leu Pro Pro Leu Gln Tyr Pro Lys Val Leu His Phe Ala Ala
 165 170 175
 Asp Ser Ile Asn Ile Asn Lys Lys Ile Trp Asn Met Tyr Phe Arg Asp
 180 185 190
 Leu Val Pro Arg Leu Val Lys Lys Gly Asp Asp Gly Asn Tyr Gly Ser
 195 200 205
 Thr Ala Val Cys Asp Ala Ile Cys Leu Gln Cys Leu Ser Lys Arg Ile
 210 215 220
 His Tyr Gly Lys Phe Val Ala Glu Ala Lys Phe Gln Ala Ser Pro Glu
 225 230 235 240

Lys	Leu	Leu	Thr	Phe	Glu	Lys	Val	Glu	Glu	Met	Val	Lys	Lys	Arg	Val
	195						200					205			
Gln	Lys	Lys	Ala	Glu	Thr	Phe	Gly	Gln	Glu	Val	Lys	Phe	Asn	Ser	Gly
	210						215				220				
Tyr	Gly	Asp	Glu	Ser	Lys	Lys	Lys	Tyr	Lys	Val	Asp	Pro	Leu	Leu	Ala
225					230					235					240
Ser	Arg	Ile	Tyr	Gly	Glu	Trp	Leu	Ile	Pro	Leu	Thr	Lys	Leu	Val	Glu
				245					250					255	
Val	Glu	Tyr	Leu	Leu	Arg	Arg	Leu	Asp							
			260					265							